SEQUENCE LISTING

<110> Bandaru, Rajasekhar
      Meyers, Rachel A.

<120> 55562 AND 21617, NOVEL HUMAN PROTEINS
      AND METHODS OF USE THEREOF

<130> 10448-123001

<150> 60/256,249
<151> 2000-12-18

<150> 60/256,405
<151> 2000-12-18

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3624
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (339)...(1361)

<400> 1

```
tagtctaact cgcggctgtc accgccactg cagcggagcc ggccggccgg gcgctgcggg      60
acgggcgggc ggctgccggc aggaggcgcc gagccgggtg actgccgcgg cgggcacagt     120
ccggggccac agcgccgagc ccgggcggga gtggccccgc gcaggcaggg agcggcgccg     180
cgcactccaa cccggcgggc acctcggggg cgggcgcggg gcgcagcctt ctcgtcccgg     240
cctctgtgac aagcgccccg gagccgggag cccgattgcc gggctcgggg tgggcgcgga     300
cgcaggcact gggctcgtgc ggggccccgg gcgtcgcg atg aac atc gtg gtg gag     356
                                            Met Asn Ile Val Val Glu
                                            1               5
```

```
ttc ttc gtg gtc act ttc aaa gtg ctc tgg gcg ttc gtg ctg gcc gcg      404
Phe Phe Val Val Thr Phe Lys Val Leu Trp Ala Phe Val Leu Ala Ala
            10              15                  20
```

```
gcg cgc tgg ctg gtg cgg ccc aag gag aag agc gtg gcg ggc cag gtg      452
Ala Arg Trp Leu Val Arg Pro Lys Glu Lys Ser Val Ala Gly Gln Val
        25                  30                  35
```

```
tgc ctc atc acc ggc gcc ggc agc ggc ctg ggc cgc ctc ttc gcg ctg      500
Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu Gly Arg Leu Phe Ala Leu
        40                  45                  50
```

```
gag ttc gcc cgg cgt cgg gcg ctg ctg gtg ctg tgg gac atc aac acg      548
Glu Phe Ala Arg Arg Arg Ala Leu Leu Val Leu Trp Asp Ile Asn Thr
55                  60                  65                  70
```

```
caa agc aac gag gag acg gct ggc atg gtg cgc cac atc tac cgc gac        596
Gln Ser Asn Glu Glu Thr Ala Gly Met Val Arg His Ile Tyr Arg Asp
             75                  80                  85

ctg gag gcg gcc gac gcc gct gcg ctg caa gct ggg aat ggt gag gaa        644
Leu Glu Ala Ala Asp Ala Ala Ala Leu Gln Ala Gly Asn Gly Glu Glu
             90                  95                 100

gaa att ctg ccc cac tgt aac ttg cag gtt ttt acc tac acc tgt gac        692
Glu Ile Leu Pro His Cys Asn Leu Gln Val Phe Thr Tyr Thr Cys Asp
            105                 110                 115

gtg ggg aag agg gag aac gtc tac ctg acg gct gaa aga gtc cgc aag        740
Val Gly Lys Arg Glu Asn Val Tyr Leu Thr Ala Glu Arg Val Arg Lys
            120                 125                 130

gag gtt ggc gaa gtc tca gtc ctg gtc aat aat gct ggt gtg gtc tct        788
Glu Val Gly Glu Val Ser Val Leu Val Asn Asn Ala Gly Val Val Ser
135                 140                 145                 150

ggg cat cac ctt ctg gaa tgt cct gat gag ctc att gag aga acc atg        836
Gly His His Leu Leu Glu Cys Pro Asp Glu Leu Ile Glu Arg Thr Met
                155                 160                 165

atg gtc aat tgc cat gca cac ttc tgg acc act aag gct ttt ctt cct        884
Met Val Asn Cys His Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro
                170                 175                 180

acg atg ctg gag att aat cat ggt cat att gtg aca gtt gca agt tcc        932
Thr Met Leu Glu Ile Asn His Gly His Ile Val Thr Val Ala Ser Ser
            185                 190                 195

ttg gga ttg ttc agt act gcc gga gtt gag gat tac tgt gcc agt aaa        980
Leu Gly Leu Phe Ser Thr Ala Gly Val Glu Asp Tyr Cys Ala Ser Lys
        200                 205                 210

ttt gga gtt gtg ggt ttt cat gaa tcc ctg agc cat gaa cta aag gct       1028
Phe Gly Val Val Gly Phe His Glu Ser Leu Ser His Glu Leu Lys Ala
215                 220                 225                 230

gct gaa aag gat gga att aaa aca acc ttg gtt tgc cct tat ctt gta       1076
Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu Val Cys Pro Tyr Leu Val
                235                 240                 245

gac act ggc atg ttc aga ggc tgc cga atc agg aaa gaa att gag cct       1124
Asp Thr Gly Met Phe Arg Gly Cys Arg Ile Arg Lys Glu Ile Glu Pro
            250                 255                 260

ttt ctg cca cct ctg aag cct gat tac tgt gtg aag cag gcc atg aag       1172
Phe Leu Pro Pro Leu Lys Pro Asp Tyr Cys Val Lys Gln Ala Met Lys
            265                 270                 275

gcc atc ctc act gac cag ccc atg atc tgc act ccc cgc ctc atg tac       1220
Ala Ile Leu Thr Asp Gln Pro Met Ile Cys Thr Pro Arg Leu Met Tyr
            280                 285                 290

atc gtg acc ttc atg aag agc atc cta cca ttt gaa gca gtt gtg tgc       1268
```

```
Ile Val Thr Phe Met Lys Ser Ile Leu Pro Phe Glu Ala Val Val Cys
295             300             305             310


atg tat cgg ttc cta gga gcg gac aag tgt atg tac ccc ttt att gct     1316
Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys Met Tyr Pro Phe Ile Ala
                315             320             325


caa aga aag caa gcc aca aac aat aat gaa gca aaa aat gga atc         1361
Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu Ala Lys Asn Gly Ile
            330             335             340


taagaatctt tttgtatgga atattacttc tatcagaaga tgatcaagat gtttcagtcc   1421
agtgcacatc agcattgctg acattttatg gattctaaac ttgtgttgtt tctttttttaa  1481
atcaactttt taaaaaaata aagtgtaaat taaccgacta gagtacttgg aaaatgtgat   1541
cagtacaagt gaacttaggt tgttgccaac agggtccttt taggcagaac ccagaaacca   1601
gtcaaatctg tagagaagca gtgtgacatc ttcaggttac cattattttt taatgagcag   1661
gaagtctaga aatgataact agactgtatg tttcatgtgt gtgatttttc agaattccca   1721
gagtttactc attcttgtta ttaaactcta gccagttgac atcttcgcaa tttcaaggac   1781
tgatagtgct gtattttctc acgttttcta agtttccgtt ttgcaaggcc taggtgactt   1841
tttcatggtg tttgtatgtt tagctctttt gaaaaggaat tttgaaatct ccatcaactg   1901
aagtaaatga tgtctgagtg ttacagtwaa ggtgaccaag tctctttctt aaagtcacaa   1961
tgactaaagt attagttgaa ttttttttttt tttttttgat ggagtctcgc tctgtcacca  2021
ggctggagtg cagtagcaca atcacggctc actgcaatct ctgcctcccr gtttcaagtg   2081
attctgctgt ctcagcctcc caagtagctg ggactacagg catcgccac cacgcccagc    2141
taattttttgt attttttagta gagacggggt ttcaccatgt tggtcaggat ggtctccatc 2201
tcttgacatt gtgatccacc tgcctcggcc tcccaaagtg ctgggattac aggcatgagc   2261
cactgcaccc agccttgaat ttttaatttt atctctgata tacttcatta agtgtctgga   2321
gacctaatta tcctaaaaga tcatacattt tctacctatg aattttgctg catacagaaa   2381
gtgccctttc ctcaggaagt tgctgtgttt catttctttg gatggactct tatctagaat   2441
acatagcagc tctgcaaaga aacagttttt aaaaatggga acttctacat tgaaaagtcc   2501
ccattttttgt gccaactatg attagtgaga ggaagaaatc ttattctatg gcatatgtat   2561
ggaagggtgt aaagattctt ttgaaaggtt tattcacatt gtagaacagc aaatgacatt   2621
tttacagtat ttttttgtaa agcaaactat tttgtgcctt gaatttggta tatgtgtatt   2681
agtgaaacat tgtaaaggtg aacttctacc tctgtatcta aatgtatacc atccacttgt   2741
aaatgactat aaactattat gtgattgctt tttttttttag aatgtcttgt ttaaatagtg  2801
gccaatgttt aaggctgtta aaataagcca actttttacta attggggagt tttataaatg   2861
actgattaaa tttaaagaat taacttacat gcaattgtgt gattattagt tatcagcagt   2921
gttgtaagga aaattattgt gttttttttt atgatcatta tcccacttta ggtaaagaaa    2981
aatattggaa tggaatagtg ttgggaaaca gacattaaca acctaggtg cctgcactca    3041
aatagccgat gttactgtcc ctagattaga gacttgatta agggcttgtt tgtaccaaaa   3101
gtggggaaac aatgccatga cctgtgtttt agtttggctg caccacagat caaatctgca   3161
ctgtgtctac atataggaaa ggtcctggtg tgtgctaatg ttcccaatgc aggacttgag   3221
gaagagctct gttatatgtt tccatttctc tttatcaaag ataaccaaac cttatggccc   3281
ttataacaat ggaggcactg gctgcctctt aattttcaat catggaccta agaagtact    3341
ctgaagggtc tcaacaatgc caggtgggga cagatatact cagagattat ccaggtctgc   3401
ctcccagcga gcctggagta caccagaccc tcctagagaa atctgttata atttaacaac   3461
ccacttatcc accttaaaac tgaggaaagt cgtctttaca tctaattttta ttcttgtgtg   3521
ttataactta aacctatttc tattttttgtt tgttattgcc cttataaggg tgtccatctc   3581
caagttcaat aaactaattc atttaaaaaa aaaaaaaaaa aaa                     3624


<210> 2
<211> 341
<212> PRT
<213> Homo sapiens


<400> 2
Met Asn Ile Val Val Glu Phe Phe Val Val Thr Phe Lys Val Leu Trp
```

```
  1                  5                      10                     15
Ala Phe Val Leu Ala Ala Ala Arg Trp Leu Val Arg Pro Lys Glu Lys
              20                      25                     30
Ser Val Ala Gly Gln Val Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu
              35                      40                     45
Gly Arg Leu Phe Ala Leu Glu Phe Ala Arg Arg Arg Ala Leu Leu Val
    50                      55                     60
Leu Trp Asp Ile Asn Thr Gln Ser Asn Glu Glu Thr Ala Gly Met Val
65                      70                     75                     80
Arg His Ile Tyr Arg Asp Leu Glu Ala Ala Asp Ala Ala Ala Leu Gln
              85                      90                     95
Ala Gly Asn Gly Glu Glu Glu Ile Leu Pro His Cys Asn Leu Gln Val
              100                     105                    110
Phe Thr Tyr Thr Cys Asp Val Gly Lys Arg Glu Asn Val Tyr Leu Thr
    115                     120                    125
Ala Glu Arg Val Arg Lys Glu Val Gly Glu Val Ser Val Leu Val Asn
    130                     135                    140
Asn Ala Gly Val Val Ser Gly His His Leu Leu Glu Cys Pro Asp Glu
145                     150                    155                    160
Leu Ile Glu Arg Thr Met Met Val Asn Cys His Ala His Phe Trp Thr
              165                     170                    175
Thr Lys Ala Phe Leu Pro Thr Met Leu Glu Ile Asn His Gly His Ile
              180                     185                    190
Val Thr Val Ala Ser Ser Leu Gly Leu Phe Ser Thr Ala Gly Val Glu
              195                     200                    205
Asp Tyr Cys Ala Ser Lys Phe Gly Val Val Gly Phe His Glu Ser Leu
    210                     215                    220
Ser His Glu Leu Lys Ala Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu
225                     230                    235                    240
Val Cys Pro Tyr Leu Val Asp Thr Gly Met Phe Arg Gly Cys Arg Ile
              245                     250                    255
Arg Lys Glu Ile Glu Pro Phe Leu Pro Pro Leu Lys Pro Asp Tyr Cys
              260                     265                    270
Val Lys Gln Ala Met Lys Ala Ile Leu Thr Asp Gln Pro Met Ile Cys
              275                     280                    285
Thr Pro Arg Leu Met Tyr Ile Val Thr Phe Met Lys Ser Ile Leu Pro
    290                     295                    300
Phe Glu Ala Val Val Cys Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys
305                     310                    315                    320
Met Tyr Pro Phe Ile Ala Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu
              325                     330                    335
Ala Lys Asn Gly Ile
              340
```

```
<210> 3
<211> 1026
<212> DNA
<213> Homo sapiens

<400> 3
atgaacatcg tggtggagtt cttcgtggtc actttcaaag tgctctgggc gttcgtgctg      60
gccgcggcgc gctggctggt gcggcccaag gagaagagcg tggcgggcca ggtgtgcctc     120
atcaccggcg ccggcagcgg cctgggccgc ctcttcgcgc tggagttcgc ccggcgtcgg     180
gcgctgctgg tgctgtggga catcaacacg caaagcaacg aggagacggc tggcatggtg     240
cgccacatct accgcgacct ggaggcggcc gacgccgctg cgctgcaagc tgggaatggt     300
gaggaagaaa ttctgcccca ctgtaacttg caggttttta cctacacctg tgacgtgggg     360
aagagggaga cgtctacct gacggctgaa agagtccgca aggaggttgg cgaagtctca     420
```

```
gtcctggtca ataatgctgg tgtggtctct gggcatcacc ttctggaatg tcctgatgag      480
ctcattgaga gaaccatgat ggtcaattgc catgcacact tctggaccac taaggctttt      540
cttcctacga tgctggagat taatcatggt catattgtga cagttgcaag ttccttggga      600
ttgttcagta ctgccggagt tgaggattac tgtgccagta aatttggagt tgtgggtttt      660
catgaatccc tgagccatga actaaaggct gctgaaaagg atggaattaa aacaaccttg      720
gtttgccctt atcttgtaga cactggcatg ttcagaggct gccgaatcag gaaagaaatt      780
gagccttttc tgccacctct gaagcctgat tactgtgtga agcaggccat gaaggccatc      840
ctcactgacc agcccatgat ctgcactccc cgcctcatgt acatcgtgac cttcatgaag      900
agcatcctac catttgaagc agttgtgtgc atgtatcggt cctaggagc ggacaagtgt      960
atgtaccct ttattgctca agaaagcaa gccacaaaca ataatgaagc aaaaaatgga     1020
atctaa                                                              1026
```

<210> 4
<211> 1327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (367)...(1188)

<400> 4

```
cctgctgcaa tggcttacgg gagccaatgt gacgggatca gggcagaccc atttagggtt      60
tcgtaaccgg ccaattcagt acgcaatagg gaaaatcaat taggatctgc agagggttcc     120
cggatacacc ttgcgaagaa tgccgcactc tccgccactc attccccact caccggcacc     180
cgctaaacct tcagcctgaa attttcctcc gaaggaagca gagcagagga agaactacca     240
agtgctacac tcaaagcctg ccgtcgcagt gagcgcgacc tccaaactga ggcattttg      300
ttccggcgaa atccctccca ctcaggaaag tccctagaaa gagagcgcag gcgcctgggg     360
tatcac atg acc act tcc cgg aag cgc agc aga ccc gct caa ctt cat      408
        Met Thr Thr Ser Arg Lys Arg Ser Arg Pro Ala Gln Leu His
         1               5                       10
```

```
cct ggg ttg agg cgg agg aga act tcc aga att atg gcg aag tcc ggg      456
Pro Gly Leu Arg Arg Arg Arg Thr Ser Arg Ile Met Ala Lys Ser Gly
 15                  20                      25                  30
```

```
ctg agg cag gac ccg cag agc aca gct gca gcc act gtg cta aag cgg      504
Leu Arg Gln Asp Pro Gln Ser Thr Ala Ala Ala Thr Val Leu Lys Arg
                    35                  40                  45
```

```
gca gta gaa cta gat tcg gag tcg cgg tat ccg cag gct ctg gtg tgt      552
Ala Val Glu Leu Asp Ser Glu Ser Arg Tyr Pro Gln Ala Leu Val Cys
                50                  55                  60
```

```
tac caa gag ggg att gat ctg ctc ctg cag gtt ctg aaa ggt acc aaa      600
Tyr Gln Glu Gly Ile Asp Leu Leu Leu Gln Val Leu Lys Gly Thr Lys
            65                  70                  75
```

```
gat aat act aag aga tgt aat ctc aga gaa aaa att tcc aaa tac atg      648
Asp Asn Thr Lys Arg Cys Asn Leu Arg Glu Lys Ile Ser Lys Tyr Met
        80                  85                  90
```

```
gac aga gcg gaa aac ata aag aag tac ttg gac caa gaa aaa gaa gat      696
Asp Arg Ala Glu Asn Ile Lys Lys Tyr Leu Asp Gln Glu Lys Glu Asp
 95                  100                 105                 110
```

```
gga aaa tat cac aag caa att aaa ata gaa gag aat gca aca ggt ttc      744
Gly Lys Tyr His Lys Gln Ile Lys Ile Glu Glu Asn Ala Thr Gly Phe
```

```
                Gly Lys Tyr His Lys Gln Ile Lys Ile Glu Glu Asn Ala Thr Gly Phe
                            115              120              125

                agt tat gag tca ctt ttt cgc gaa tac ctt aat gag aca gtt aca gaa      792
                Ser Tyr Glu Ser Leu Phe Arg Glu Tyr Leu Asn Glu Thr Val Thr Glu
                            130              135              140

                gtt tgg ata gaa gat cct tat att aga cat act cat cag ctg tat aac      840
                Val Trp Ile Glu Asp Pro Tyr Ile Arg His Thr His Gln Leu Tyr Asn
                            145              150              155

                ttt ctt cga ttt tgt gag atg ctt att aag aga cca tgt aaa gta aaa      888
                Phe Leu Arg Phe Cys Glu Met Leu Ile Lys Arg Pro Cys Lys Val Lys
                            160              165              170

                act att cac ctt ctc acc tct ctg gat gaa ggc att gag caa gtg cag      936
                Thr Ile His Leu Leu Thr Ser Leu Asp Glu Gly Ile Glu Gln Val Gln
                175              180              185              190

                caa agt aga ggc ctg caa gaa ata gaa gag tca ctc agg agt cac gga      984
                Gln Ser Arg Gly Leu Gln Glu Ile Glu Glu Ser Leu Arg Ser His Gly
                            195              200              205

                gtg ctg ttg gaa gtt caa tac tct tct tca ata cat gac cga gaa att     1032
                Val Leu Leu Glu Val Gln Tyr Ser Ser Ser Ile His Asp Arg Glu Ile
                            210              215              220

                agg ttc aac aat gga tgg atg att aag att gga agg gga ctt gat tat     1080
                Arg Phe Asn Asn Gly Trp Met Ile Lys Ile Gly Arg Gly Leu Asp Tyr
                            225              230              235

                ttt aag aaa cca cag agt cgt ttt tcc ctt gga tat tgt gat ttt gat     1128
                Phe Lys Lys Pro Gln Ser Arg Phe Ser Leu Gly Tyr Cys Asp Phe Asp
                            240              245              250

                tta aga cca tgt cat gaa aca aca gta gac att ttt cat aag aag cat     1176
                Leu Arg Pro Cys His Glu Thr Thr Val Asp Ile Phe His Lys Lys His
                255              260              265              270

                aca aaa aat ata tgatgggtgg tagcctaatt tgtattatgt ctactttaag        1228
                Thr Lys Asn Ile


                tgaatattgg attttttta aaagatcact tttataatgt atgaatttaa caataaactt     1288
                ttatatttct actaaaaaaa aaaaaaaaa aaaaaaaaa                            1327
```

<210> 5
<211> 274
<212> PRT
<213> Homo sapiens

<400> 5

```
Met Thr Thr Ser Arg Lys Arg Ser Arg Pro Ala Gln Leu His Pro Gly
1               5                   10                  15
Leu Arg Arg Arg Arg Thr Ser Arg Ile Met Ala Lys Ser Gly Leu Arg
                20                  25                  30
Gln Asp Pro Gln Ser Thr Ala Ala Ala Thr Val Leu Lys Arg Ala Val
```

```
                  35                       40                       45
Glu Leu Asp Ser Glu Ser Arg Tyr Pro Gln Ala Leu Val Cys Tyr Gln
        50                       55                       60
Glu Gly Ile Asp Leu Leu Leu Gln Val Leu Lys Gly Thr Lys Asp Asn
65                       70                       75                       80
Thr Lys Arg Cys Asn Leu Arg Glu Lys Ile Ser Lys Tyr Met Asp Arg
                85                       90                       95
Ala Glu Asn Ile Lys Lys Tyr Leu Asp Gln Glu Lys Glu Asp Gly Lys
            100                      105                      110
Tyr His Lys Gln Ile Lys Ile Glu Glu Asn Ala Thr Gly Phe Ser Tyr
        115                      120                      125
Glu Ser Leu Phe Arg Glu Tyr Leu Asn Glu Thr Val Thr Glu Val Trp
    130                      135                      140
Ile Glu Asp Pro Tyr Ile Arg His Thr His Gln Leu Tyr Asn Phe Leu
145                      150                      155                      160
Arg Phe Cys Glu Met Leu Ile Lys Arg Pro Cys Lys Val Lys Thr Ile
                165                      170                      175
His Leu Leu Thr Ser Leu Asp Glu Gly Ile Glu Gln Val Gln Gln Ser
            180                      185                      190
Arg Gly Leu Gln Glu Ile Glu Glu Ser Leu Arg Ser His Gly Val Leu
        195                      200                      205
Leu Glu Val Gln Tyr Ser Ser Ser Ile His Asp Arg Glu Ile Arg Phe
    210                      215                      220
Asn Asn Gly Trp Met Ile Lys Ile Gly Arg Gly Leu Asp Tyr Phe Lys
225                      230                      235                      240
Lys Pro Gln Ser Arg Phe Ser Leu Gly Tyr Cys Asp Phe Asp Leu Arg
                245                      250                      255
Pro Cys His Glu Thr Thr Val Asp Ile Phe His Lys Lys His Thr Lys
            260                      265                      270
Asn Ile
```

<210> 6
<211> 825
<212> DNA
<213> Homo sapiens

<400> 6

```
atgaccactt cccggaagcg cagcagaccc gctcaacttc atcctgggtt gaggcggagg       60
agaacttcca gaattatggc gaagtccggg ctgaggcagg acccgcagag cacagctgca      120
gccactgtgc taaagcgggc agtagaacta gattcggagt cgcggtatcc gcaggctctg      180
gtgtgttacc aagaggggat tgatctgctc ctgcaggttc tgaaaggtac caaagataat      240
actaagagat gtaatctcag agaaaaaatt tccaaataca tggacagagc ggaaaacata      300
aagaagtact tggaccaaga aaaagaagat ggaaaatatc acaagcaaat taaaatagaa      360
gagaatgcaa caggtttcag ttatgagtca ctttttcgcg aataccttaa tgagacagtt      420
acagaagttt ggatagaaga tccttatatt agacatactc atcagctgta taactttctt      480
cgattttgtg agatgcttat taagagacca tgtaaagtaa aaactattca ccttctcacc      540
tctctggatg aaggcattga gcaagtgcag caaagtagag gcctgcaaga aatagaagag      600
tcactcagga gtcacggagt gctgttggaa gttcaatact cttcttcaat acatgaccga      660
gaaattaggt tcaacaatgg atggatgatt aagattggaa ggggacttga ttattttaag      720
aaaccacaga gtcgtttttc ccttggatat tgtgattttg atttaagacc atgtcatgaa      780
acaacagtag acattttttca taagaagcat acaaaaaata tatga                      825
```

<210> 7
<211> 206
<212> PRT
<213> Artificial Sequence

```
<220>
<223> Consensus sequence

<400> 7
Lys Val Ala Leu Val Thr Gly Ala Ser Ser Gly Ile Gly Leu Ala Ile
1               5                   10                  15
Ala Lys Arg Leu Ala Lys Glu Gly Ala Lys Val Val Val Ala Asp Arg
            20                  25                  30
Asn Glu Glu Lys Leu Glu Lys Gly Ala Val Ala Lys Glu Leu Lys Glu
                35                  40                  45
Leu Gly Gly Asn Asp Lys Asp Arg Ala Leu Ala Ile Gln Leu Asp Val
            50                  55                  60
Thr Asp Glu Glu Ser Val Lys Ala Ala Val Glu Gln Ala Val Glu Arg
65                  70                  75                  80
Leu Gly Arg Gly Leu Asp Val Leu Val Asn Asn Ala Gly Gly Ile Ile
                85                  90                  95
Leu Leu Arg Pro Gly Pro Phe Ala Glu Leu Ser Arg Thr Met Glu Glu
            100                 105                 110
Asp Trp Asp Arg Val Ile Asp Val Asn Leu Thr Gly Val Phe Leu Leu
            115                 120                 125
Thr Arg Ala Val Leu Pro Leu Met Ala Met Lys Lys Arg Gly Gly Gly
            130                 135                 140
Arg Ile Val Asn Ile Ser Ser Val Ala Gly Arg Lys Glu Gly Gly Leu
145                 150                 155                 160
Val Gly Val Pro Gly Gly Ser Ala Tyr Ser Ala Ser Lys Ala Ala Val
                165                 170                 175
Ile Gly Leu Thr Arg Ser Leu Ala Leu Glu Leu Ala Pro His Gly Gly
            180                 185                 190
Ile Arg Val Asn Ala Val Ala Pro Gly Gly Val Asp Thr Asp
            195                 200                 205

<210> 8
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 8
Ala Glu Ala Tyr Tyr Asn Leu Gly Asn Ala Tyr Leu Lys Leu Gly Lys
1               5                   10                  15
Tyr Asp Glu Ala Ile Glu Asp Tyr Glu Lys Ala Leu Glu Leu Asp Pro
            20                  25                  30
Asn Asn

<210> 9
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 9
```

ner